



### AMENDMENTS TO THE CLAIMS

This listing of the claims replaces all prior listings and versions:

1-23. (canceled).

24. (currently amended) A plant host cell or transgenic plant comprising

(i) a polynucleotide encoding a zinc finger polypeptide comprising at least two zinc fingers, each zinc finger comprising a binding motif comprising the amino acid sequence shown in

~~X<sup>a</sup>-C X<sub>2-4</sub>-C X<sub>3</sub>-F X<sup>e</sup>-X X X X L X X H X X X<sup>b</sup>-H~~ linker (SEQ ID NO: 22)

~~wherein each of X, X<sup>a</sup>, X<sup>b</sup>, X<sup>e</sup> is any amino acid, the numbers in subscript indicate possible numbers of residues, and X X X X L X X H X X between X<sup>e</sup> and X<sup>b</sup> are designated positions 1, 1, 2, 3, 4, 5, 6, 7, 8, and 9; and~~

(ii) a target DNA sequence,

wherein at least one binding motif has been engineered to bind to the target DNA sequence.

25. (canceled)

26. (canceled)

27. (currently amended ) The plant host cell or transgenic plant of claim ~~26~~ 24 wherein X<sup>a</sup> the amino acid residue at position 1 of SEQ ID NO:22 is E, K, T, S, Q, V, A or P, X<sup>b</sup> the amino acid residue at position 23 of SEQ ID NO:22 is T or I, X<sup>e</sup> the amino acid residue at position 12 of SEQ ID NO:22 is S or T, X<sub>2-4</sub> there are two amino acids at positions 3-6 of SEQ ID NO:22 is two amino acids, with the first of which being S, E, K, T, P, or R, and the second amino acid being E, and wherein the two zinc finger proteins are linked by the sequence shown in the linker is T-G-E-K (SEQ ID NO: 23) or T-G-E-K-P (SEQ ID NO: 24), and the amino acid residue at position 9 21 of SEQ ID NO:22 is Arg or Lys, and the amino acid residues at positions ~~1, 5 and 8~~ 14, 18 and 21 of SEQ ID NO:22 are hydrophobic amino acids and not Phe, Trp or Tyr.

28. (currently amended) The plant host cell or transgenic plant of claim ~~26~~ 24 wherein one or more the zinc fingers binds to a target DNA triplet in accordance with the following:

(a) if the 5' base in the triplet is G, then position ~~6~~ 19 of SEQ ID NO:22 of the first zinc finger is Arg or position [[++2]] 15 of SEQ ID NO:22 of the second zinc finger is Asp or position ~~6~~ 19 of SEQ ID NO:22 of the first zinc finger is Arg and position ~~6~~ 19 of SEQ ID NO:22 of the first zinc finger is Asp;

(b) if the 5' base in the triplet is A, then position ~~6~~ 19 of SEQ ID NO:22 of the first zinc finger is Gln or Glu and [[++2]] position 15 of SEQ ID NO:22 of the second zinc finger is not Asp;

(c) if the 5' base in the triplet is T, then position ~~6~~ 19 of SEQ ID NO:22 of the first zinc finger is Ser or Thr and position [[++2]] 15 of SEQ ID NO:22 of the second zinc finger is Asp or position ~~6~~ 19 of SEQ ID NO:22 of the first zinc finger is a hydrophobic amino acid other than Ala;

(d) if the 5' base in the triplet is C, then position ~~6~~ 19 of SEQ ID NO:22 of the first zinc finger may be any amino acid, provided that position [[++2]] 15 of SEQ ID NO:22 of the second zinc finger is not Asp;

(e) if the central base in the triplet is G, then position ~~3~~ position 16 of SEQ ID NO:22 is His;

(f) if the central base in the triplet is A, then position ~~3~~ position 16 of SEQ ID NO:22 is Asn;

(g) if the central base in the triplet is T, then position ~~3~~ position 16 of SEQ ID NO:22 is Ala, Ser, Ile, Leu, Thr or Val provided that if it is Ala, then one of the residues at [[ -1]] position 13 or 6 position 19 of SEQ ID NO:22 is a small residue;

(h) if the central base in the triplet is 5-meC, then position ~~3~~ position 16 of SEQ ID NO:22 is Ala, Ser, Ile, Leu, Thr or Val provided that if it is Ala, then one of the residues at [[ -1]] position 13 or 6 position 19 of SEQ ID NO:22 is a small residue;

(i) if the 3' base in the triplet is G, then position [[ -1]] position 13 is Arg;

(j) if the 3' base in the triplet is A, then position [[ -1]] position 13 is Gln and position 2 15 of SEQ ID NO:22 is Ala;

(k) if the 3' base in the triplet is T, then position ~~[[ -1]]~~ position 13 is Asn or position ~~[[ -1]]~~ position 13 is Gln and position ~~2~~ 15 of SEQ ID NO:22 is Ser;

(l) if the 3' base in the triplet is C, then position ~~[[ -1]]~~ position 13 is Asp and position ~~1~~ 14 of SEQ ID NO:22 is Arg;

and,

when the central residue of a target triplet is C, the use of Asp at position ~~3~~ position 16 of SEQ ID NO:22 allows preferential binding to C over 5-mC; ~~and,~~

~~wherein “++” residues are residues present in a C terminal adjacent zinc finger, and when there is no C terminal adjacent zinc finger, “++” interactions do not operate.~~

29. (currently amended) The plant host cell or transgenic plant of claim ~~26~~ 24 wherein there is an N-terminal zinc finger having a leader peptide ~~MAEEKP~~ as shown in (SEQ ID NO: ~~27~~) added thereto.

30. (withdrawn-currently amended) The plant host cell or transgenic plant of claim ~~25~~ 24 wherein one or more of the zinc fingers of the polypeptide comprises a mutated model zinc finger domain.

31. (withdrawn) The plant host cell or transgenic plant of claim 30 wherein the model zinc finger domain is a zinc finger from a protein selected the group consisting of Zif268, GLI, Tramtrack, or YY1.

32. (currently amended) The plant host cell or transgenic plant of claim ~~25~~ 24, wherein the zinc finger polypeptide has more than three zinc fingers.

33. (previously presented) The plant host cell or transgenic plant of claim 32 wherein the zinc finger polypeptide has four, five, six, seven, eight or nine zinc fingers.

34. (canceled)

**35.** (previously presented) The plant host cell or transgenic plant of claim 24, wherein the target DNA sequence is operably linked to a coding sequence.

**36.** (previously presented) The plant host cell or transgenic plant of claim 35, wherein transcription of the coding sequence is regulated by binding of the zinc finger polypeptide to the target DNA sequence.

**37.** (previously presented) The plant host cell or transgenic plant of claim 24, wherein the target DNA sequence is part of an endogenous sequence.

**38.** (previously presented) The plant host cell or transgenic plant of claim 35, wherein the target DNA sequence and the coding sequence are heterologous to the cell.

**39.** (previously presented) The plant host cell or transgenic plant of claim 24, wherein the zinc finger polypeptide is fused to a transcriptional activator domain.

**40.** (canceled)

**41.** (previously presented) The plant host cell or transgenic plant of claim 39 wherein the transcriptional activator domain comprises a VP16 transcriptional activator domain.

**42.** (previously presented) The plant host cell or transgenic plant of claim 39 wherein the transcriptional activator domain comprises a VP64 transcriptional activator domain.

**43.** (withdrawn) The plant host cell or transgenic plant of claim 24, wherein the zinc finger polypeptide is fused to a transcriptional repressor domain.

**44-47.** (canceled)

**48.** (previously presented) The plant host cell of claim 24, wherein the zinc finger polypeptide is fused to a catalytic domain of a restriction enzyme.

**49.** (previously presented) The plant host cell or transgenic plant of claim 24 which is a transgenic plant.

**50.** (previously presented) The plant host cell or transgenic plant of claim 24 which is a plant host cell.

**51 to 70.** (canceled).

**71.** (previously presented) The plant host cell or transgenic plant of claim 24, wherein the second His residue is replaced by Cys.